

STIC-Biotechnology Systems Branch

RAW SEQUENCE LISTING

ERROR REPORT

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The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

10/555,583

Source:

PCT

Date Processed by STIC:

12/01/2005

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT,

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/533, 583

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to 3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7 Skipped Sequences
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
(NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

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PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/555,383

DATE: 12/01/2005

TIME: 14:09:03

Input Set : N:\Rasheed\Sequence Listing 03500.102556.txt

Output Set: N:\CRF4\12012005\J555383.raw

3 <110> APPLICANT: Ban, Kazuhiro
 4 Shiotsuka, Hidenori
 5 Imamura, Takeshi
 7 <120> TITLE OF INVENTION: Kit for immobilizing organic substance, organic substance immobilized
 8 structure, and manufacturing methods therefor
 11 <130> FILE REFERENCE: 03500.102556
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/555,383
 C--> 14 <141> CURRENT FILING DATE: 2005-11-03
 16 <150> PRIOR APPLICATION NUMBER: JP2004-016858
 17 <151> PRIOR FILING DATE: 2004-01-26
 19 <160> NUMBER OF SEQ ID NOS: 181
 21 <170> SOFTWARE: MS-WORD

Does Not Comply
 Corrected Diskette Needed

(pg-1,2,3,4,5)

ERRORED SEQUENCES

275 <210> SEQ ID NO: 22
 276 <211> LENGTH: 12
 277 <212> TYPE: PRT
 278 <213> ORGANISM: Artificial Sequence
 280 <220> FEATURE:
 281 <223> OTHER INFORMATION: anodisk membrane-binding peptide
 283 <400> SEQUENCE: 22
 284 Met Lys Thr His His Gly Asn Asn Ala Val Phe Leu
 E--> 285 1 (1) 5 (5) 10 (10)
 383 <210> SEQ ID NO: 31
 384 <211> LENGTH: 10
 385 <212> TYPE: PRT
 386 <213> ORGANISM: Artificial Sequence
 388 <220> FEATURE:
 389 <223> OTHER INFORMATION: anodisk membrane-binding peptide
 391 <400> SEQUENCE: 31
 392 Ala Cys Asn Gly Met Leu Ala Phe Gln Cys
 E--> 393 1 5 (5) 10 (10)
 537 <210> SEQ ID NO: 35
 538 <211> LENGTH: 559
 539 <212> TYPE: PRT
 540 <213> ORGANISM: Pseudomonas cichorii YN2 ; FERM BP-7375
 542 <400> SEQUENCE: 35
 543 Met Ser Asn Lys Ser Asn Asp Glu Leu Lys Tyr Gln Ala Ser Gly Asn
 E--> 544 1 5 10 (10) 15 (15)
 546 Thr Leu Gly Leu Asn Pro Val Val Gly Leu Arg Gly Lys Asp Leu Leu
 E--> 547 20 (20) 25 (25) 30 (30)

Insufficient Explanation.
 What is the source of
 genetic material?
 Pls see Glem# 11 on
 error summary sheet.

Invalid
 Amino acid
 numbering
 Pls see
 Glem# 3
 on error
 summary
 sheet.

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RAW SEQUENCE LISTING

DATE: 12/01/2005

PATENT APPLICATION: US/10/555-383

TIME: 14:09:03

Input Set: N:\Rasheed\Sequence Listing\03500.102556.txt

Output Set: N:\CRF4\12012005\J555383.raw

549 Ala Ser Ala Arg Met Val Leu Arg Gln Ala Ile Lys Gln Pro Val His
 E--> 550 65 35 40 40 45 45
 552 Ser Val Lys His Val Ala His Phe Gly Leu Glu Leu Lys Asn Val Leu
 E--> 553 50 50 55 55 60 60
 555 Leu Gly Lys Ser Gly Leu Gln Pro Thr Ser Asp Asp Arg Arg Rhe Ala
 E--> 556 65 65 70 70 75 75 80
 558 Asp Pro Ala Trp Ser Gln Asn Pro Leu Tyr Lys Arg Tyr Leu Gln Thr
 E--> 559 80 85 90 95
 561 Tyr Leu Ala Trp Arg Lys Glu Leu His Asp Trp Ile Asp Glu Ser Asn
 E--> 562 100 105 110
 564 Leu Ala Pro Lys Asp Val Ala Arg Gly His Phe Val Ile Asn Leu Met
 E--> 565 115 120 125
 567 Thr Glu Ala Met Ala Pro Thr Asn Thr Ala Ala Asn Pro Ala Ala Val
 568 130 135 140
 570 Lys Arg Phe Phe Glu Thr Gly Gly Lys Ser Leu Leu Asp Gly Leu Ser
 E--> 571 145 150 155 160
 573 His Leu Ala Lys Asp Leu Val His Asn Gly Gly Met Pro Ser Gln Val
 E--> 574 165 170 175
 576 Asn Met Gly Ala Phe Glu Val Gly Lys Ser Leu Gly Val Thr Glu Gly
 E--> 577 180 185 190
 579 Ala Val Val Phe Arg Asn Asp Val Leu Glu Leu Ile Gln Tyr Lys Pro
 E--> 580 195 200 205
 582 Thr Thr Glu Gln Val Tyr Glu Arg Pro Leu Leu Val Val Pro Pro Gln
 E--> 583 210 215 220
 585 Ile Asn Lys Phe Tyr Val Phe Asp Leu Ser Pro Asp Lys Ser Leu Ala
 586 225 230 235 240
 588 Arg Phe Cys Leu Arg Asn Asn Val Gln Thr Phe Ile Val Ser Trp Arg
 E--> 589 245 250 255
 591 Asn Pro Thr Lys Glu Gln Arg Glu Trp Gly Leu Ser Thr Tyr Ile Glu
 E--> 592 260 265 270
 594 Ala Leu Lys Glu Ala Val Asp Val Val Thr Ala Ile Thr Gly Ser Lys
 E--> 595 275 280 285
 597 Asp Val Asn Met Leu Gly Ala Cys Ser Gly Gly Ile Thr Cys Thr Ala
 E--> 598 290 295 300
 600 Leu Leu Gly His Tyr Ala Ala Ile Gly Glu Asn Lys Val Asn Ala Leu
 601 305 310 315 320
 603 Thr Leu Leu Val Ser Val Leu Asp Thr Thr Leu Asp Ser Asp Val Ala
 E--> 604 325 330 335
 606 Leu Phe Val Asn Glu Gln Thr Leu Glu Ala Ala Lys Arg His Ser Tyr
 E--> 607 340 345 350
 609 Gln Ala Gly Val Leu Glu Gly Arg Asp Met Ala Lys Val Phe Ala Trp
 E--> 610 355 360 365
 612 Met Arg Pro Asn Asp Leu Ile Trp Asn Tyr Trp Val Asn Asn Tyr Leu
 E--> 613 370 375 380
 615 Leu Gly Asn Glu Pro Pro Val Phe Asp Ile Leu Phe Trp Asn Asn Asp
 E--> 616 385 390 395 400
 618 Thr Thr Arg Leu Pro Ala Ala Phe His Gly Asp Leu Ile Glu Leu Phe
 E--> 619 405 410 415
 621 Lys Asn Asn Pro Leu Ile Arg Pro Asn Ala Leu Glu Val Cys Gly Thr

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Same Error

RAW SEQUENCE LISTING

DATE: 12/01/2005

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TIME: 14:09:03

Input Set: N:\Rasheed\Sequence Listing_03500.102556.txt

Output Set: N:\CRF4\12012005\J555383.raw

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```

E--> 622          420          425          430
624 Pro Ile Asp Leu Lys Gln Val Thr Ala Asp Ile Phe Ser Leu Ala Gly
625          435          440          445
627 Thr Asn Asp His Ile Thr Pro Trp Lys Ser Cys Tyr Lys Ser Ala Gln
628          450          455          460
630 Leu Phe Gly Gly Asn Val Glu Phe Val Leu Ser Ser Ser Gly His Ile
E--> 631 465          470          475          480
633 Gln Ser Ile Leu Asn Pro Pro Gly Asn Pro Lys Ser Arg Tyr Met Thr
E--> 634          485          490          495
636 Ser Thr Glu Val Ala Glu Asn Ala Asp Glu Trp Gln Ala Asn Ala Thr
E--> 637          500          505          510
639 Lys His Thr Asp Ser Trp Trp Leu His Trp Gln Ala Trp Gln Ala Gln
E--> 640          515          520          525
642 Arg Ser Gly Glu Leu Lys Lys Ser Pro Thr Lys Leu Gly Ser Lys Ala
E--> 643          530          535          540
645 Tyr Pro Ala Gly Glu Ala Ala Pro Gly Thr Tyr Val His Glu Arg
646 545          550          555
648 <210> SEQ ID NO: 36
649 <211> LENGTH: 560
650 <212> TYPE: PRT
651 <213> ORGANISM: Pseudomonas cichorii YN2 ; FERM BP-7375
653 <400> SEQUENCE: 36
654 Met Arg Asp Lys Pro Ala Arg Glu Ser Leu Pro Thr Pro Ala Lys Phe
655 1          5          10          15
657 Ile Asn Ala Gln Ser Ala Ile Thr Gly Leu Arg Gly Arg Asp Leu Val
658          20          25          30
660 Ser Thr Leu Arg Ser Val Ala Ala His Gly Leu Arg His Pro Val His
E--> 661          35          40          45
663 Thr Ala Arg His Ala Leu Lys Leu Gly Gly Gln Leu Gly Arg Val Leu
E--> 664          50          55          60
666 Leu Gly Asp Thr Leu His Pro Thr Asn Pro Gln Asp Arg Arg Phe Asp
E--> 667 65          70          75          80
669 Asp Pro Ala Trp Ser Leu Asn Pro Phe Tyr Arg Arg Ser Leu Gln Ala
E--> 670          85          90          95
672 Tyr Leu Ser Trp Gln Lys Gln Val Lys Ser Trp Ile Asp Glu Ser Asn
673          100          105          110
675 Met Ser Pro Asp Asp Arg Ala Arg Ala His Phe Ala Phe Ala Leu Leu
E--> 676          115          120          125
678 Asn Asp Ala Val Ser Pro Ser Asn Ser Leu Leu Asn Pro Leu Ala Ile
E--> 679          130          135          140
681 Lys Glu Ile Phe Asn Ser Gly Gly Asn Ser Leu Val Arg Gly Ile Gly
682 145          150          155          160
684 His Leu Val Asp Asp Leu Leu His Asn Asp Gly Leu Pro Arg Gln Val
E--> 685          165          170          175
687 Thr Arg His Ala Phe Glu Val Gly Lys Thr Val Ala Thr Thr Thr Gly
E--> 688          180          185          190
690 Ala Val Val Phe Arg Asn Glu Leu Leu Glu Leu Ile Gln Tyr Lys Pro
E--> 691          195          200          205
693 Met Ser Glu Lys Gln Tyr Ser Lys Pro Leu Leu Val Val Pro Pro Gln

```

Serial Error

RAW SEQUENCE LISTING

DATE: 12/01/2005

PATENT APPLICATION: US/10/555,383

TIME: 14:09:03

Input Set: N:\Rasheed\Sequence Listing-03500-102556.txt

Output Set: N:\CRF4\12012005\J555383.raw

E--> 694 210 215 220
 696-Ile Asn-Lys-Tyr Tyr-Ile Phe-Asp-Leu-Ser-Pro-His Asn-Ser-Phe Val
 697 225 230 235 240
 699 Gln Phe Ala Leu Lys Asn Gly Leu Gln Thr Phe Val Ile Ser Trp Arg
 E--> 700 245 250 255
 702 Asn Pro Asp Val Arg His Arg Glu Trp Gly Leu Ser Thr Tyr Val Glu
 E--> 703 260 265 270
 705 Ala Val Glu Glu Ala Met Asn Val Cys Arg Ala Ile Thr Gly Ala Arg
 E--> 706 275 280 285
 708 Glu Val Asn Leu Met Gly Ala Cys Ala Gly Gly Leu Thr Ile Ala Ala
 E--> 709 290 295 300
 711 Leu Gln Gly His Leu Gln Ala Lys Arg Gln Leu Arg Arg Val Ser Ser
 E--> 712 305 310 315 320
 714 Ala Thr Tyr Leu Val Ser Leu Leu Asp Ser Gln Leu Asp Ser Pro Ala
 E--> 715 325 330 335
 717 Thr Leu Phe Ala Asp Glu Gln Thr Leu Glu Ala Ala Lys Arg Arg Ser
 E--> 718 340 345 350
 720 Tyr Gln Lys Gly Val Leu Glu Gly Arg Asp Met Ala Lys Val Phe Ala
 E--> 721 355 360 365
 723 Trp Met Arg Pro Asn Asp Leu Ile Trp Ser Tyr Phe Val Asn Asn Tyr
 E--> 724 370 375 380
 726 Leu Met Gly Lys Glu Pro Pro Ala Phe Asp Ile Leu Tyr Trp Asn Asn
 E--> 727 385 390 395 400
 729 Asp Asn Thr Arg Leu Pro Ala Ala Leu His Gly Asp Leu Leu Asp Phe
 E--> 730 405 410 415
 732 Phe Lys His Asn Pro Leu Ser His Pro Gly Gly Leu Glu Val Cys Gly
 E--> 733 420 425 430
 735 Thr Pro Ile Asp Leu Gln Lys Val Thr Val Asp Ser Phe Ser Val Ala
 736 435 440 445
 738 Gly Ile Asn Asp His Ile Thr Pro Trp Asp Ala Val Tyr Arg Ser Thr
 739 450 455 460
 741 Leu Leu Leu Gly Gly Glu Arg Arg Phe Val Leu Ala Asn Ser Gly His
 E--> 742 465 470 475 480
 744 Val Gln Ser Ile Leu Asn Pro Pro Asn Asn Pro Lys Ala Asn Tyr Leu
 E--> 745 485 490 495
 747 Glu Gly Ala Lys Leu Ser Ser Asp Pro Arg Ala Trp Tyr Tyr Asp Ala
 E--> 748 500 505 510
 750 Lys Pro Val Asp Gly Ser Trp Trp Thr Gln Trp Leu Gly Trp Ile Gln
 E--> 751 515 520 525
 753 Glu Arg Ser Gly Ala Gln Lys Glu Thr His Met Ala Leu Gly Asn Gln
 E--> 754 530 535 540
 756 Asn Tyr Pro Pro Met Glu Ala Ala Pro Gly Thr Tyr Val Arg Val Arg
 757 545 550 555 560
 2390 <210> SEQ ID NO: 172
 2391 <211> LENGTH: 16
 2392 <212> TYPE: PRT
 2393 <213> ORGANISM: Artificial Sequence
 2395 <220> FEATURE:
 2396 <223> OTHER INFORMATION: anodisk membrane-binding peptide

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Same Error

Same Error

RAW SEQUENCE LISTING

DATE: 12/01/2005

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TIME: 14:09:03

Input Set: N:\Rasheed\Sequence Listing_03500:102556.txt

Output Set: N:\CRF4\12012005\J555383.raw

2398 <400> SEQUENCE: 172

2399 Val Tyr Ala Asn Gln Thr Pro Pro Ser Arg Ala Arg Ala Lys Ala Arg

E--> 2400 1 5 10 15

2402 <210> SEQ ID NO: 173

2403 <211> LENGTH: 20

2404 <212> TYPE: PRT

2405 <213> ORGANISM: Artificial Sequence

2407 <220> FEATURE:

2408 <223> OTHER INFORMATION: anodisk membrane-binding peptide

2410 <400> SEQUENCE: 173

2411 Val Tyr Ala Asn Gln Thr Pro Pro Ser Lys Ala Arg Tyr Ala Gln

E--> 2412 1 5 10 15

2413 Thr Pro Pro Ser Arg

2414 20

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↑

If no errors shown exist then
please listing. Please check
sequences for similar errors.

VERIFICATION SUMMARY

DATE: 12/01/2005

PATENT APPLICATION: US/10/555,383

TIME: 14:09:04

Input Set: N:\Rasheed\Sequence Listing 03500-102556.txt

Output Set: N:\CRF4\12012005\J555383.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application Number

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:285 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22

L:393 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:31

L:411 M:283 W: Missing Blank Line separator, <220> field identifier

L:475 M:283 W: Missing Blank Line separator, <220> field identifier

L:544 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35

L:547 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35

L:550 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35

L:553 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35

L:556 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35

L:559 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35

L:562 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35

L:565 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35

L:571 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35

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L:577 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35

L:580 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35

L:583 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35

L:589 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35

L:592 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35

L:595 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35

L:598 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35

L:604 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35

L:607 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35

L:610 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35

L:613 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35

L:616 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35

L:619 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35

L:622 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35

L:631 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35

L:634 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35

L:637 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35

L:640 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35

L:643 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35

L:661 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36

L:664 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36

L:667 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36

L:670 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36

L:676 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36

L:679 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36

L:685 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36

L:688 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36

L:691 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36

L:694 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36

L:700 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36

L:703 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36

L:706 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36

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VERIFICATION SUMMARY

DATE: 12/01/2005

PATENT APPLICATION: US/10/555,383

TIME: 14:09:04

Input Set: N:\Rasheed\Sequence Listing-03500-102556.txt

Output Set: N:\CRF4\12012005\J555383.raw

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L:712 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
L:715 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
L:718 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
L:721 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
L:724 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
L:727 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
L:730 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
L:733 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
L:742 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
L:745 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
L:748 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
L:751 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
L:754 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
L:2400 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:172
L:2412 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:173

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